



# AK

LOCUS AF134837 2982 bp DNA linear BCT 14-OCT-1999

DEFINITION Amycolatopsis mediterranei aspartokinase and aspartate-semialdehyde dehydrogenase operon, complete sequence.

ACCESSION AF134837

VERSION AF134837.1 GI:5733410

KEYWORDS

SOURCE Amycolatopsis mediterranei

ORGANISM Amycolatopsis mediterranei

Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;

Pseudonocardineae; Pseudonocardiaceae; Amycolatopsis.

REFERENCE 1 (bases 1 to 2982)

AUTHORS Zhang,W., Jiang,W., Zhao,G., Yang,Y. and Chiao,J.

TITLE Sequence analysis and expression of the aspartokinase and aspartate semialdehyde dehydrogenase operon from rifamycin SV-producing amycolatopsis mediterranei

JOURNAL Gene 237 (2), 413-419 (1999)

PUBMED 10521665

REFERENCE 2 (bases 1 to 2982)

AUTHORS Zhang,W., Jiang,W.H., Zhao,G.P., Yang,Y.L. and Chiao,J.S.

TITLE Direct Submission

JOURNAL Submitted (13-MAR-1999) Microbiology. Shanghai Institute of Plant Physiology, Academia Sinica, 300 Fenglin Road, Shanghai, SH 200032, P.R.China

FEATURES	Location/Qualifiers
source	1..2982 /organism="Amycolatopsis mediterranei" /mol_type="genomic DNA" /strain="U32" /db_xref="taxon:33910"
gene	220..2525 /gene="aspartokinase and aspartate-semialdehyde dehydrogenase operon"
gene	220..1485

CDS 220..1485

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/transl\_table=11

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/db\_xref="GI:5733411"

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 DTTDELLDLAQVNPAPPEREMDMLLTAGERISNSLVAMAIAAQGAWSFTGSQAGV  
 VTTSVHGNARIIDVTPSRVTEALDQGYIALVAGFQGVADTKDITTLGRGGSDDTAVA  
 LAAALNADVCEIYSDVDGVYTADPRVVPDAKKLDTVTYEEMLELAASGSKILHLSVE  
 YARRYGVPIRVRSYSDKPGTTVTGSIEEIPVEQALITGVAHDRSEAKITVTGVPDHT  
 GAAARIFRVIADAEIDIDMVLQNVSSSTVSGRTDITFTLSKANGAKAVKELEKVQAEIG  
 FESVLYDDHVGKVSVVGAGMRSHPGVTATFCEALAEAGVNIEINTSEIRISVLIRDA  
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CDS 967..1485

/gene="askA"

/note="Orf2"

/codon\_start=1

/transl\_table=11

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/translation="MEQALITGVAHDRSEAKITVTGVPDHTGAAARIFRVIADAEIDI  
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CDS 1485..2525

/note="Orf3"

/codon\_start=1

/transl\_table=11

/product="aspartate-semialdehyde dehydrogenase"

/protein\_id="AAD49569.1"

/db\_xref="GI:5733413"

/translation="MADGLRVGVVGATGQVGAVMRKLLAEREFFIAELRYFASARSAG"

SKLPWRDTEITIEDASTADPSGLDIALFSAGGSTSKAQAPRFAAAGVTVIDNSSAFRM  
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 SGSGLAGVDELAGQVRAAAEHASLLTHDGAIDFPKPEKYVRPIAFNVLPMAGSIVDD  
 GEFETDEEKKFRNESRKILSIPGLAVSCTCVRVPVFSGHSVSVNAEFERPLSVERATE  
 LLTHAPGVELSEPTPLQAAGNDPSYVGRIRVDPGVEGGRGLALFLSNDNLRKGAALN  
 AIQIAELVAQQL"

# ORIGIN

1 ggtaccgcg tgtgtgtgc atcactcggg aggaagggt ccgcgcattt cgttggtgtt  
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 121 gggccgcga agccccgta ggctcctgt caaatcatgg gacgggggg ctcctcgtg  
 181 cccaccaggg agcccccgg cccgcgagga ggttcgggg tggccctcgt ggtccagaag  
 241 tacggcggtat cgtcgtgga aagtccgac cggatcaagc gcgtggcgga gcggtcgtc  
 301 gcgacgaaga aggggggcaa cgacgtcgtc gtcgtcgtc cggcgatggg tgacaccacc  
 361 gacgagctgc tcgacctggc gcagcaggtc aaccggcgc gcgcggagcg ggagatggac  
 421 atgtgtctca ccgcgggtga gcgcatctcg aactcgtgg tcgcatggc gatcgggcc  
 481 caggcgcccg aggcgtggc gttcacgggt tcgaggccg gcgtcgtac gacgtcgtg  
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 1261 tcggtggtc gcgcgggat gcgtcgcac ccgggtgtca cggcgaggt ctgcgaagcg  
 1321 ctggccgagg ccggcgtaa catcgaaatc atcaacacct cggagatccg cattcgggtg  
 1381 ctgatccgc acgcgcagct cgacgacgc gtgcgcgca tccacgaggc attcgaactc  
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 1561 agcgggagtt cccgatcgc gagctgcgt acttcgctc ggccgctcg gcggggtcga  
 1621 aacttcgtg gcgtgacac gaaatcaga tcgaggacgc ctcgacggcg gatccgtccg  
 1681 gtttgacat cgcgtgttc tcggcggcg gtcgacgtc gaaggcgag gccccgggt

1741 tcgccgcggc cggggtcacg gtgatcgaca actcgtcggc gttccggatg gacccggacg  
 1801 tgccgtgggt cgtcagcgag gtcaatcccg aggctgtcaa ggaagcgcgc aaggggatca  
 1861 tcggaatcc caactgcacc acgatcgccg cgtgccggt gctgaagccg ctgcacgacg  
 1921 aggcggcctt ggtccgctg gtcgcgtcga cgtaccaggc ggtgtccggc agcgggctgg  
 1981 ccggcgtcga cgagctgcc gggcagggtc gggcgggcgc cgagcacgca tcgtctcga  
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 2401 tccggtgga cccgggtgtc gaggcgggc gcgggtcgc gctgttctc tcgaacgaca  
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 2521 tctgacgacc acgcgaagg cccctaccg agcgcggtga gggccaacg cgtgaattca  
 2581 cggccgggtt gcgcgtagc aggcgaggtg gcgcgtcttc aggaactcgc gttccggcgc  
 2641 gccggttag gccagacga gcgcgtccg gtgcacgcc agcacctga actgctcgac  
 2701 ggcctcgtc caccggtcgt tcgccaccg tgccttggc gcgtacgcgc ggtcgcggag  
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 2821 cttggtcgg tcgtcttcc aggcgcgac gccctgttc tccgttctg gcgcggcgac  
 2881 gagcgtagg cccgcagct tcgggcctt gtcgaggct tcgtcggcga acggaacat  
 2941 ctgctcgtc gagccgaacc attggcgca ccagtactgc ag

//

[ GENETYX : Amino Acid Sequence Homology Data ]

Date : 2005.06.09

1st Amino Acid Sequence

File Name : Amycolatopsis mediterranei\_askA.prj  
Sequence Size : 421

2nd Amino Acid Sequence

File Name : M.methylotrophus ask.prj  
Sequence Size : 409

Unit Size to Compare = 2  
Pick up Location = 1

[49.633% / 409 aa] INT/OPT.Score : < 285/ 982 >

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1" MALIVQKYGG TSVANPERIR NVARRVARYK ALGHQVVVVV SAMSGETNRL ISLAKEIMQD PDPRELDVMV

71' TAGERISNSL VAMAIQAQA EAWSFTGSQA GVVTTSVHGN ARIIDVTPSR VTEALDQGYI ALVAGFQGVA
..*... ..*..* * *..*..* ..*... ..*... ..*...*..*..* ..*...*..*
71" STGEQVTIGM TALALMELGI KAKSYTGTQV KILTDDAFTK ARILDIDEHN LKKDLDDGYV CVVAGFQGVV

141' QDTKDITTLG RGGSDTTAVA LAAALNADVC EIYSDVDGVY TADPRVVPDA KKLDTVTYEE MLELAASGSK
... ..***** ..*****. ** ..*****. * ..*****. * ..*****. * ..*****. ***
141" ANG-NITTLG RGGSDTTGVA LAAALKADEC QIYTDVDGVY TTDPRVPEA RRLDKITFEE MLELASQGSK

211' ILHLRSVEYA RRYGVPIRVR SSYSK-PGT TVTGSIEEIP VEQALITGVA HDRSEAKITV TGVPDHTGAA
..*...*..* * *..*..* ..*... ** *..*..* ..*...*..* ..*...*..* ..*...*..*
210" VLQIRSEFEA GKYKVKLRVL SSFEEEGDGT LITFEENEEN MEEPIISGIA FNRDEAKITV TGVPDKPGIA

280' ARIFRVIADA EIDIDMVLQN VSSTVSGRTD ITFTLSKANG AKAVKEL-EK VQAEIGFESV LYDDHVGKVS
..*...*..* ..*...*..* *... *..*..* ..*...*..* ..*...*..* ..*...*..* ..*...*..*
280" YQILGPVADA NIDVDMIQN VGAD--GTTD FTFTVHKNEK NKALSILRDK VQGHQIAREI SGDDKIAKVS

349' VVGAGMRSHP GVTATFCEAL AEAGVNIEII NTSEIRISVL IRDAQLDDAV RAIHEAFELG GDEEAVVYAG
***.***** *... ..*..*..*..* ..*...*..* *... ..*..* ..*...*..*
348" VVGVMRSHV GIASQMFRITL AEEGINIQMI STSEIKIAVV IEEKYMELAV RVLHKAFFLE NA
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# AK-2

AL162756. Reports *Neisseria meningi...*[gi:7380091] Links

LOCUS NMA5Z2491 1218 bp DNA linear BCT 16-APR-2005

DEFINITION *Neisseria meningitidis* serogroup A strain Z2491 complete genome;  
segment 5/7.

ACCESSION AL162756 REGION: complement(298368..299585)

VERSION AL162756.2 GI:7380091

KEYWORDS

SOURCE *Neisseria meningitidis* Z2491

ORGANISM *Neisseria meningitidis* Z2491

Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales;

Neisseriaceae; *Neisseria*.

REFERENCE 1 (bases 1 to 1218)

AUTHORS Parkhill,J., Achtman,M., James,K.D., Bentley,S.D., Churcher,C.,

Klee,S.R., Morelli,G., Basham,D., Brown,D., Chillingworth,T.,

Davies,R.M., Davis,P., Devlin,K., Feltwell,T., Hamlin,N.,

Holroyd,S., Jagels,K., Leather,S., Moule,S., Mungall,K.,

Quail,M.A., Rajandream,M.A., Rutherford,K.M., Simmonds,M.,

Skelton,J., Whitehead,S., Spratt,B.G. and Barrell,B.G.

TITLE Complete DNA sequence of a serogroup A strain of *Neisseria*  
*meningitidis* Z2491

JOURNAL Nature 404 (6777). 502-506 (2000)

PUBMED 10761919

REFERENCE 2 (bases 1 to 1218)

AUTHORS Parkhill,J.

TITLE Direct Submission

JOURNAL Submitted (30-MAR-2000) Submitted on behalf of the *Neisseria*  
sequencing team, Sanger Centre, Wellcome Trust Genome Campus,  
Hinxton, Cambridge CB10 1SA E-mail: parkhill@sanger.ac.uk

COMMENT Notes:

Details of *N. meningitidis* sequencing at the Sanger Centre are  
available on the World Wide Web.

(URL, [http://www.sanger.ac.uk/Projects/N\\_meningitidis/](http://www.sanger.ac.uk/Projects/N_meningitidis/)).

FEATURES	Location/Qualifiers
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gene	1..1218 /gene="lysC"
CDS	1..1218 /gene="lysC" /EC_number="2.7.2.4" /note="NMA1701, lysC, aspartate kinase, len: 405aa; similar to many eg. SW:P26512 (AKAB_CORGL) lysC, aspartate kinase from Corynebacterium glutamicum (Brevibacterium flavum) (421 aa) fasta scores; E0: 0, 49.6% identity in 409 aa overlap. Contains Pfam match to entry PF00696 aakinese, Aspartate kinases, Glutamate kinases and Gamma glutamate phospho-reductases and Prosite match to PS00324 Aspartokinase signature." /codon_start=1 /transl_table=11 <u>/product="aspartate kinase"</u> /protein_id="CAB84929.1" /db_xref="GI:7380342" /db_xref="GOA:Q9JTN3" /db_xref="InterPro:IPR001048" /db_xref="InterPro:IPR001057" /db_xref="InterPro:IPR001341" /db_xref="InterPro:IPR002912" /db_xref="InterPro:IPR005260" /db_xref="UniProt/TrEMBL:Q9JTN3" /translation="MALIVHKYGGTSVGSPERIKNVAKRVAKARAEGHDIVVVVSAMS GETNRLVALAHEMQEHPDPRELDVVLSTGEQVTIGLLAMALKDIGVDAKSYTGWQVAL KTDTAHTKARIESIDDEKMRADLTAGKVTVVAGFQGISEGDISTLGRGSDTSAVAL AAALKADECQIYTDVDGVYTTDPRVVPEARRMDTVTFEEMIELASLGSKVLQIRSVEF

AGKYKVRRLRVLSSLQDGGNGTLITFEEDDNMERA AVT GIAFDKNQARINVRGVDPKPG  
 VAYQILGAVADANIEVDMIIQNVGSEGTTDFSFTVPRGDYKQTLEILSERQDSIGAAS  
 IDGDDTVCKVSAVGLGMRSHVGVAAKIFRTLAEEGINIQMISTSEIKVSVLIDEKYME  
 LATRVLHKAFNLG"

misc\_feature 13..39  
 /gene="lysC"  
 /note="PS00324 Aspartokinase signature."  
 misc\_feature 205..882  
 /gene="lysC"  
 /note="Pfam match to entry PF00696 aakinase, Aspartate  
 kinases, Glutamate kinases and Gamma glutamate  
 phospho-reductases, score 114.30, E-value 2.3e-30"

#### ORIGIN

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 121 tccgccatga gcggtgaaac caaccgcctg gtcgcgttgg cgcacgaaat gcaggagcat  
 181 cccgatccgc gcgaattgga cgtggtttg tccaccggcg aacaagtaac catcggcctt  
 241 ttggcgatgg cattgaaaga catcggcgtg gatccaaaa gctacacagg ctggcaggtc  
 301 gccctcaaaa ccgataccgc ccacacaaa gcccgcatcg aaagcattga tgacgaaaaa  
 361 atgcgtgccg accttaccgc cggcaaagtc gtcacgttg ccggcttcca aggcacacgc  
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 661 aagtacaaag tgcgcctcgc cgtactgagc agcctgcaag acggcggcaa tggcacctta  
 721 attacctttg aagaggacga caacatggaa agagctgccg taaccgggat cgcattcgat  
 781 aaaaaccaag cccgcaccaa cgtgcgcggc gtacccgaca aaccgggtgt cgcctatcag  
 841 attttggcgc cggtcgccga tgccaacatc gaagtgcata tgattatcca aaatgtcggc  
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 961 gaaatcctgt cggaacgcca agacagtatc ggcgcggcct ctattgatgg cgacgacacc  
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 1081 atcttcgcga cgctgccga agagggtatc aacatccaaa tgatttcac ctccgaaatc  
 1141 aaagtttcgc tattgattga tgaaaaatc atggaactgg caaccagggt attgcataaa  
 1201 gcctttaatt tgggctga

//



[ GENETYX : Amino Acid Sequence Homology Data ]

Date : 2005.06.09

1st Amino Acid Sequence

File Name : Neisseria meningitidis\_ask.prj  
Sequence Size : 405

2nd Amino Acid Sequence

File Name : MM.prj  
Sequence Size : 409

Unit Size to Compare = 2

Pick up Location = 1

[70.197% / 406 aa] INT/OPT.Score : < 870/ 1400 >

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1' MALIVHKYGG TSVGSPERIK NVAKRVAKAR AEGHDIVVVV SAMSGETNRL VALAHEMQEH PDPRELDVVL
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1" MALIVQKYGG TSVANPERIR NVARRVARYK ALGHQV VVVV SAMSGETNRL ISLAKEIMQD PDPRELDVMV

71' STGEQVTIGL LAMALKDIGV DAKSYTGWQV ALKTDTAHTK ARIESIDDEK MRADLTAGKV VIVAGFQGIS
***** **..**..**.. ***** ** ..**.* ** **..**.. **..**.* *****..
71" STGEQVTIGM TALALMELGI KAKSYTGTQV KILTDDAFTK ARILDIDEHN LKKDLDDGYV CVVAGFQGVV

141' SEGDISTLGR GGSDTSAVAL AAALKADECQ IYTDVGVYV TDPRVVPEAR RMDTVTFEEM IELASLGSKV
**.*.***** *****..** ***** ***** ***** **..***** *****
141" ANGNITTLGR GGSDDTGVAL AAALKADECQ IYTDVGVYV TDPRVVPEAR RLDKITFEEM LELASQGSKV

211' LQIRSVFAG KYKVLRLVLS SLQDGGNGTL ITFEE-DDNM ERAAVTGIAF DKNQARINVR GVPDKPGVAY
***** ***** **..**.* ***** ***** **..***** **..**.* *****..**
211" LQIRSVFAG KYKVLRLVLS SFEEEGDGTI ITFEENEENM EEPIISGIAF NRDEAKITVT GVPDKPGIAY

280' QILGAVADAN IEVDMIIQNV GSEGTDFSF TVPRGDYKQT LEILSER-QD SIGAASIDGD DTVCKVSAVG
****.***** *.***** **..***** **..**..**.. **..**..**.. **..**.* **..**.*
281" QILGPVADAN IDVDMIIQNV GADGTTDFTF TVHKNEMNKA LSILRDKVQG HIQAREISGD DKIAKVSVVG

349' LGMRSVGVGA AKIFRTLAE GINIQMISTS EIKVSVLIDE KYMELATRVL HKAFNLG
*****.* **..***** ***** ***** **..**.* *****.* *****.*
351" VGMRSVGVGA SQMFRTLAE GINIQMISTS EIKIADVIEE KYMELAVRVL HKAFGLENA

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# DDPS

1: AF065159. Reports Bradyrhizobium ja...[gi:6655022] Links

LOCUS AF065159 891 bp DNA linear BCT 03-JAN-2000

DEFINITION Bradyrhizobium japonicum putative arylsulfatase (arsA), putative soluble lytic transglycosylase precursor (sltA), dihydrodipicolinate synthase (dapA), MscL (mscL), SmpB (smpB), BcpB (bcpB), RnpO (rnpO), RelA/SpoT homolog (relA), PdxJ (pdxJ), and acyl carrier protein synthase AcpS (acpS) genes, complete cds; prokaryotic type I signal peptidase SipF (sipF) gene, sipF-sipS allele, complete cds; RNase III (rnc), GTP-binding protein Era (era), hypothetical protein, recO-like protein, topoisomerase II (gyrA), putative ABC transporter, putative GMC-oxidoreductase, hypothetical protein, putative cytochrome C binding protein (cyc4), putative polytopic integral membrane protein, superoxide dismutase SodM-like protein, putative inner membrane protein, AttM-like protein (attM), adenylate cyclases-like protein, and putative inner membrane protein (spcT) genes, complete cds; and unknown genes.

ACCESSION AF065159 REGION: 4811..5701

VERSION AF065159.3 GI:6655022

KEYWORDS

SOURCE Bradyrhizobium japonicum

ORGANISM Bradyrhizobium japonicum

Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;

Bradyrhizobiaceae; Bradyrhizobium.

REFERENCE 1 (bases 1 to 891)

AUTHORS Mueller,P. and Stingel,D.

TITLE Extended DNA sequencing in the upstream region of sipF in  
Bradyrhizobium japonicum

JOURNAL Unpublished

REFERENCE 2 (bases 1 to 891)

AUTHORS Mueller,P. and Stingel,D.

TITLE Direct Submission

JOURNAL Submitted (27-OCT-1999) Biology, Philipps Universitaet Marburg.

Karl-von-Frisch-Strasse, Marburg 35032, Germany

REMARK Sequence update by submitter

REFERENCE 3 (bases 1 to 891)

AUTHORS Mueller,P. and Stingel,D.

TITLE Direct Submission

JOURNAL Submitted (03-JAN-2000) Biology, Philipps Universitaet Marburg,

Karl-von-Frisch-Strasse, Marburg 35032, Germany

REMARK Sequence update by submitter

COMMENT On Jan 3, 2000 this sequence version replaced gi:6136295.

FEATURES Location/Qualifiers

source 1..891

/organism="Bradyrhizobium japonicum"

/mol\_type="genomic DNA"

/strain="USDA 110spc4"

/db\_xref="taxon:375"

gene 1..891

/gene="dapA"

CDS 1..891

/gene="dapA"

/function="involved in the biosynthesis of the rhizopine

3-O-methyl-scylo-inosamine"

/function="catalyzes the first step in the biosynthesis of  
diaminopimelate and lysine from aspartate semialdehyde"

/note="similar to the MosA protein of Sinorhizobium  
meliloti; belongs to the DHDPs family"

/codon\_start=1

/transl\_table=11

/product="dihydrodipicolinate synthase"

/protein\_id="AAF04320.1"

/db\_xref="GI:6136299"

/translation="MAAKTKFRGSFTALVTPFKNGSLDEAAFRSLVNWQISEGTNGLV

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AVLVVTPYYNKPTQEGMYQHFKAINDAIGIPHIYNIPPRSVIDMSVDTMKRLWELKN

IAGVKDATASMRVRSQQRAAMGEDFNQLSGEVATILGYMAQCGHGCISVTSNVAPRLC

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VTEPTRVAVRSAMVHAGLIN"

## ORIGIN

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121 aacggactgg tcccggctgg cagcacaggc gagagccga cgtcagcca tgacgagcac  
181 aagaaggtcg tcgagtggcg catcgaggag gccaagggcc gcgtgcccggt ggttgcgggt  
241 gccggctcca actcgaccaa ggaggcgatc gagctggccc agcacgccga gaaggcgggc  
301 gcggacgccg tgctgggtgt gacgccttac tacaacaagc cgaccagga agggatgtac  
361 cagcattca aggcgatcaa cgatgcgatc gggattcaa tcatattta caacatccc  
421 ccgcgctcgg tgatcgacat gtcggtcgac accatgaagc ggctgtggga gctgaagaac  
481 atcggcgccg tcaaggacgc caccgcagc atggtccgcg tctcgagca gcgtgccgcg  
541 atggcgaggg acttcaacca gctctcgggc gaggtagcga ccactcctgg ctacatggcc  
601 caatcgggcc acggctgcat ctgggtgacc tgaacgtcg caccgcgcct gtgctcggag  
661 ttccacaccg cctggcagaa gggcgatcaa cgcaccgcgc tgaagctgca cgacaagctg  
721 atgcccgctg acaacaacct cttcatcgag agcaatccgg cgccgatcaa gtacgcgatg  
781 tcgctgctcg gcaagcttga cgagacgtg cggctgccga tgggtccggt gaccgagcca  
841 acgcgcgttg cgtgcgcag cgccatggtt cacgtggcc tgatcaactg a

//

[ GENETYX : Amino Acid Sequence Homology Data ]

Date : 2005.06.09

1st Amino Acid Sequence

File Name : Bradyrhizobium japonicum\_DDPS.prj  
Sequence Size : 296

2nd Amino Acid Sequence

File Name : M.methylotrophus DDPS.prj  
Sequence Size : 296

Unit Size to Compare = 2

Pick up Location = 1

[45.329% / 289 aa] INT/OPT.Score : < 229/ 614 >

```

1' MAAKTKFRGS FTALVTP-FK NGSLDEAAFR SLVNWQISEG TNGLVPVGTG GESPTLSHDE HKKVVEWCIE
  . ** ..**.*. * .**.*. *.. ..**.*.*. *..* **..**.*. ** * .. **
1" MALGMLTGS LVAIVTPMFE DGRDLDAK KLVDFHVEAG TDGIVIVGTG GESPTVDVDE HCLLIKTIE

70' EAKGRVPVVA GAGSNSTKEA IELAQAHEKA GADAVLVVTP YYNKPTQEGM YQHFKAINDA IGIPIIIYNI
  .. **.*.*. *..**.*. ** ..**.*.*. **.*.*.*. **.*.*.*. **.*.*.*. **.*.*.*.
70" HVAKRVPVIA GTGANSTAEA IELTAKAKAL GADACLLVAP YYNKPSQEGM YQHFKAIAEA VDIPIILYNV

140' PPRSVIDMSV DTMKRLWELK NIAGVKDATA SMVRVSQORA AMGEDFNQLS GEVATILGYM AQCGHGCISV
  * * . * * **.*.*. **.*.*.*. .. * .. **.*.*. * * . * * * * * * * * *
140" PGRTGCDLSN DTVLRLAQIR NIVGIKDATG GIERGTDLLL RAPADFAIYS GDDATALALM LLGGKGVISV

210' TSNVAPRLCS EFHTAWQKGD QRTALKLHDK LMPVHNNLFI ESNPAPIKYA MSLLGKLDDE LRLPMVPVTE
  *..**.*.*. *..*.*. *..*.*. *..**.*.*. *..**.*.*. *..**.*.*. *..**.*.*.
210" TANVAPKLMH EMCEHALNGN LAAAKAANAK LFALHQLFV EANPIPVKVV LQQMGMIATG IRLPLVNLSS

280' PTRVAVRSAM VHAGLIN
  . . . . * . * . * .
280" QYHEVLRNAM KQAEIAA
  
```

# DDPS-2

NC\_003116. Reports *Neisseria meningi...*[gi:15793034] Links

LOCUS NC\_003116 876 bp DNA linear BCT 19-MAY-2005

DEFINITION *Neisseria meningitidis* Z2491, complete genome.

ACCESSION NC\_003116 REGION: complement(1073966..1074841)

VERSION NC\_003116.1 GI:15793034

KEYWORDS

SOURCE *Neisseria meningitidis* Z2491

ORGANISM *Neisseria meningitidis* Z2491

Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales;

Neisseriaceae; *Neisseria*.

REFERENCE 1 (bases 1 to 876)

AUTHORS Parkhill,J., Achtman,M., James,K.D., Bentley,S.D., Churcher,C.,

Klee,S.R., Morelli,G., Basham,D., Brown,D., Chillingworth,T.,

Davies,R.M., Davis,P., Devlin,K., Feltwell,T., Hamlin,N.,

Holroyd,S., Jagels,K., Leather,S., Moule,S., Mungall,K.,

Quail,M.A., Rajandream,M.A., Rutherford,K.M., Simmonds,M.,

Skelton,J., Whitehead,S., Spratt,B.G. and Barrell,B.G.

TITLE Complete DNA sequence of a serogroup A strain of *Neisseria meningitidis* Z2491

JOURNAL Nature 404 (6777), 502-506 (2000)

PUBMED 10761919

REFERENCE 2 (bases 1 to 876)

AUTHORS

CONSRM NCBI Genome Project

TITLE Direct Submission

JOURNAL Submitted (27-SEP-2001) National Center for Biotechnology Information, NIH, Bethesda, MD 20894, USA

REFERENCE 3 (bases 1 to 876)

AUTHORS Parkhill,J.

TITLE Direct Submission

JOURNAL Submitted (30-MAR-2000) Sanger Centre, Wellcome Trust Genome Campus, Hinxton, Cambridge CB10 1SA, United Kingdom

COMMENT PROVISIONAL REFSEQ: This record has not yet been subject to final  
NCBI review. The reference sequence was derived from AL157959.

COMPLETENESS: full length.

FEATURES	Location/Qualifiers
source	1..876 /organism="Neisseria meningitidis Z2491" /mol_type="genomic DNA" /db_xref="taxon:122587" /serogroup="A"
gene	1..876 /gene="dapA" /locus_tag="NMA1124" /db_xref="GeneID:907093"
CDS	1..876 /gene="dapA" /locus_tag="NMA1124" /EC_number="4.2.1.52" /codon_start=1 /transl_table=11 <u>/product="dihydrodipicolinate synthase"</u> /protein_id="NP_283893.1" /db_xref="GI:15794071" /db_xref="CDD:pfam00701" /db_xref="COG:COG0329" /db_xref="GeneID:907093" /translation="MLQGSLVALITPMNQDGSIHYEQLRDLIDWHIENGTDGIVAVGT TGESATLSVEEHTAVIEAVVKHVAKRVPVIAGTGANNVTVEAIALSQAAEKAGADYTLS VVPYYNKPSQEGMYRHFKAFAEAAAIPMILYNVPGRTVVSMNNETILRLAEIPNIVGV KEASGNIGSNIELINRAPEGFVVLSGDDHTALPFMLCGGHGVITVAANAAPKLFADMC RAALQGDIALARELNDRLLPIYDTMFCEPSAAPKWAVSALGRCEPHVRLPLVPLTEG GQAKVRAALKASGQL"

#### ORIGIN

```
1 atgttacaag gtagcctggt tgccctgatt accccgatga atcaagacgg cagcatccat
61 tacgaacaac tccgcgactt aatcgactgg cacattgaaa acggcagga cgcatcgtc
121 gccgtcgga cgacaggcga atccgccacc ctctccgtcg aagaacacac cgccgtcatc
181 gaagccgtcg tcaaacacgt tgccaaacgc gtccccgtca tcgccggcac aggggcaaac
```

11

Date : 2005.06.09

```
File Name      : Neisseria meningitidis_DDPS.prj
Sequence Size  : 291
```

```
File Name      : MM+4.prj
Sequence Size  : 296
```

```
Unit Size to Compare = 2
Pick up Location      = 1
```

```

1'      MLOGSL VALITPMNQD GSIHYEQLRD LIDWHIENG T DGIVAVGTTG ESATLSVEEH TAVIEAVVKH
      ** *** **.****.* *...*.**.* **.**** **.****
1"      MALGMLTGSL VAIVTPMFED GRDLDLALKK LVDFHVEAGT DGIVIVGTTG ESPTVDVDEH CLLIKTTIEH

67'     VAKRVPVIAG TGANNTVEAI ALSQAAEKAG ADYTLVVVPY YNKPSQEGMY RHFKAVAEAA AIPMILYNVP
***** **.**** **.* **.* **.**** *****.* *****.* *****
71"     VAKRVPVIAG TGANSTAEAI ELTAKAKALG ADACLLVAPY YNKPSQEGLY QHFKAVAEAV DIPQILYNVP

137'    GRTVVMNNE TILRLAEIPN IVGKEASGN IGSNIELINR APEGFVVLGS DDHTALPFML CGGHGVITVA
*** **.* **.****.* **.****.* **.****.* **.****.* **.****.*
141"    GRTGCDLSDN TVLRLAQIRN IVGIKDATGG IERGTDLLLR APADFAIYSG DDATAALALML LGGKGVISVT

207'    ANAAPKLFAD MCRAALQGDI ALARELNDR L IPIYDTMFCE PSPAAPKWAV SALGRCEPHV RLPLVPLTEG
**.****.* **.****.* **.****.* **.****.* **.****.* **.****.*
211"    ANVAPKLMHE MCEHALNGNL AAKAANAKL FALHQKLFVE ANPIPVKWVL QQMGMATGI RLPLVNLSSQ

277'    GQAKVRAALK ASGQL
      ..*.*.*
281"    YHEVLRNAMK QAEIAA

```



[ GENETYX : Amino Acid Sequence Homology Data ]

Date : 2005.05.30

1st Amino Acid Sequence

File Name : M.methylotrophus DDPS.prj  
Sequence Size : 296

2nd Amino Acid Sequence

File Name : Eshcherichia coli DDPS.prj  
Sequence Size : 292

Unit Size to Compare = 2  
Pick up Location = 1

[55.326% / 291 aa] INT/OPT.Score : < 733/ 801 >

```

1'  MALGMLTGSL  VAIVTPMFED  GRLDLDALKK  LVDFHVEAGT  DGIVIVGTTG  ESPTVDVDEH  CLLIKTTIEH
    *.*.*.*.  *.*.*.*.*.  *.*.*.*.*.  *.*.*.*.*.  *.*.*.*.*.  *.*.*.*.*.  *.*.*.*.*.
1"   MFTGSI  VAIVTPMDEK  GNVCRASLKK  LIDYHVASGT  SAIVSVGTTG  ESATLNHDEH  ADVVMTLIDL

71'  VAKRVPVIAG  TGANSTAEAI  ELTAKAKALG  ADACLLVAPY  YNKPSQEGLY  QHFKAFAEAV  DIPQILYNVP
    ..*.*.*.*.  *.*.*.*.*.  *.*.*.*.*.  *.*.*.*.*.  *.*.*.*.*.  *.*.*.*.*.  *.*.*.*.*.
67"  ADGRIPVIAG  TGANATAEAI  SLTQRFNDGS  IVGCLTVTPY  YNRPSQEGLY  QHFKAIAEHT  DLPQILYNVP

141'  GRTGCDLSND  TVLRLAQIRN  IVGIKDATGG  IERGTDLALL  APADFAIYSG  DDATALALML  LGGKGVISVT
    .*.*.*.*.  .*.*.*.*.*.  *.*.*.*.*.  *.*.*.*.*.  *.*.*.*.*.  *.*.*.*.*.  *.*.*.*.*.
137"  SRTGCDLLPE  TVGRLAKVKN  IIGIKEATGN  LTRVNQIKEL  VSDDFVLLSG  DDASALDFMQ  LGGHGVISVT

211'  ANVAPKIMHE  MCEHALNGNL  AAAKAANAAL  FALHQKLFVE  ANPIPVKWL  QQMGMIATG-  IRLPLVNLSS
    *.*.*.*.  *.*.*.*.*.  *.*.*.*.*.  *.*.*.*.*.  *.*.*.*.*.  *.*.*.*.*.  *.*.*.*.*.
207"  ANVAARDMAQ  MCKLAAEGHF  AEARVINQRL  MPLHNKLFVE  PNPIPVKWAC  KELGILVATDT  LRLPMTPTTD

280'  QYHEVLRNAM  KQAEIAA
    .*.*.*.*.  *.*.*.*.

277"  SGRETVRAAL  KHAGLL

```

[ GENETYX : Amino Acid Sequence Homology Data ]

Date : 2005.05.30

1st Amino Acid Sequence

File Name : M.methylotrophus-lysCaa.prj  
Sequence Size : 409

2nd Amino Acid Sequence

File Name : Escherichia coli-lysC.prj  
Sequence Size : 449

[26.849% / 365 aa] INT/OPT.Score : < 119/ 321 >

1'		MALIV QKYGGTSVAN PERIRNVARR
1"	MSEIVVSKFG GTSVADFDM NRSADIVLSD ANVRLVVLVA SAGITNLLVA LAEGLEPGER FEKLDAIRNI	
26'	VARYKALGHQ VVVVVSAMSG ETNRLISLAK EIMQDDPRE LDVMVSTGEQ VTIGMTALAL MELGIKAKSY	
71"	QFAILERLRY PNVIREEIER LLENITVIAE AAALATSPAL TDELVSHGEL MSTLLFVEIL RERDVQAQWF	
96'	TGTQVKILTD DAFTK----- ARILDIDEHN LKKDLDDGYV CVVAGFQGV D ANGNITTLGR GGSDDTTGVAL	
141"	DVRKV-MRTN DRFGRAEPDI AALAEALALQ LLPRINEGLV -ITQGFICSE NKGRTTTTLGR GGSDDYTAALL	
161'	AAALKADECQ IYTDVDGVYT TDPVVVPEAR RLDKITFEEM LELASQSKV LQIRSVVEFAG KYKVKLRVLS	
209"	AEALHASRVD IWTDVPGIYT TDPVVVSAK RIDEIAFAEA AEMATFGAKV LHPATLLPAV RSDIPVFGVS	
231'	SFEEEGDGL ITFEENEENM EEPISGIAF NRDEAKITVT GVP--DKPGI AYQILGPVAD ANIDVDMIIQ	
279"	SKDPRAGGTL VC----NKTE NPPLFRALAL RRNQTLLTLH SLNMLHSRGF LAEVFGILAR HNISVDLIT-	
299'	NVGADGTTDF TFTVHKNEMN KALSILRDV QGHIOAR-EI SGDDKIAKVS VVGVMRSHV GIASQMFTL	
344"	--TSEVSVAL TLDT-TGSTS TGDITLLTQSL LMELSALCRV EVEEGLALVA LIGNDLSKAC GVGKEVFGVL	
368'	AEEGINIQMI STSEIKIAVV IEKYMELAV RVLHKAFGLE NA	
411"	EPFNIRMICY GASSHNLCFL VPGEDAEQVV QKLHSLNLF	